



IN THE CLAIMS

Please amend the claims as follows. See the attached Appendix for markings to affect such amendments. All the pending claims currently under consideration have been reproduced below.

1. (Three Times Amended) An isolated nucleic acid molecule comprising at least 300 contiguous bases from an rpoB sequence selected from the group consisting of SEQ ID NOS: 2-10.

2. (Three Times Amended) The isolated nucleic acid molecule of claim 1 comprising a rpoB sequence selected from the group consisting of SEQ ID NOS: 2-10.

3. (Three Times Amended) A probe perfectly complementary to a rhoP sequence selected from the group consisting of SEQ ID NOS: 2-10.

4. (Three Times Amended) A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria;

determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid;

comparing the determined sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2-10;

classifying the mycobacteria from the extent of similarity of the compared sequences.

5. (As Filed) The method of claim 4, wherein at least 100 contiguous bases are determined from the target nucleic acid.

6. (Three Times Amended) The method of claim 4, wherein the determined sequence is compared with at least nine sequences selected from the group consisting of SEQ ID NOS: 2-10.

7. (Three Times Amended) A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid;

determining the identity of one or more bases in the target sequence at one or more positions corresponding to one or more bases in a sequence selected from the group consisting of SEQ ID NOS: 2-10 when the sequences are maximally aligned, wherein the one or more bases of the sequence selected from the group consisting of SEQ ID NOS: 2-10 differ from the corresponding one or more bases in SEQ ID NO 1 when the sequences are

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maximally aligned, the identity of the one or more bases characterizing the species of mycobacteria that is present in the sample;

comparing the identified one or more bases in the target sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2-10;

classifying the mycobacteria from the extent of similarity between the one or more bases identified in the target sequence and the corresponding one or more bases in the compared sequences.

Concluded
8. (Three Times Amended) The method of claim 7, wherein the identity of at least 10 bases in the target nucleic acid at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2-10 is determined.

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9. (Twice Amended) The method of claim 8, wherein the identity of at least 20 bases in the target sequence at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2-10 are identified.

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10. (Three Times Amended) The method of claim 9, further comprising comparing the 20 determined bases with 20 bases occupying corresponding positions in each of at least nine sequences selected from the group consisting of SEQ ID NOS: 2-10.

11. (Three Times Amended) A sequence-specific polynucleotide probe or primer that hybridizes under stringent hybridization conditions to at least a segment of a mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2-10 or its complement without hybridizing to the M. tuberculosis sequence of SEQ ID NO: 1 or its complement, wherein the segment includes at least 20 bases of a sequence selected from the group consisting of SEQ ID NOS: 2-10 which differ from the corresponding bases in SEQ ID NO 1 when the sequences are maximally aligned.

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12. (Twice Amended) The sequence-specific polynucleotide of claim 11 that is a probe.

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13. (Four Times Amended) The sequence-specific polynucleotide of claim 12, wherein a central position of the probe aligns with the one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2-10 which differ from the corresponding one or more bases in SEQ ID NO 1 when the sequences are maximally aligned.

~~13~~ 14. (Amended) The sequence-specific polynucleotide of claim 11 that is a primer.

~~D10~~ 15. (Four Times Amended) The sequence-specific polynucleotide of claim 14, wherein the 3' end of the primer aligns with the one or more bases of a sequence selected from the group consisting of SEQ ID NOS. 2-10 which differ from the corresponding one or more bases in SEQ ID NO 1 when the sequences are maximally aligned.

~~D11~~ 16. (Twice Amended) The sequence-specific polynucleotide of claim 11 that hybridizes under stringent hybridization conditions to at least 300 contiguous bases of a mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2-10 or its complement without hybridizing to the M. tuberculosis sequence of SEQ ID NO: 1 or its complement.